

=====

Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2010; month=6; day=17; hr=11; min=7; sec=24; ms=56;]

=====

Reviewer Comments:

<110> APPLICANT: Novartis AG

<120> TITLE OF INVENTION: Organic Compound

<130> FILE REFERENCE: 4-32761P1/UNZ

<140> CURRENT APPLICATION NUMBER:10538201

<141> CURRENT FILING DATE:2006-03-08

<160> NUMBER OF SEQ ID NOS: 48

<170> SOFTWARE: PatentIn version 3.1

Please remove all subject line headers from the entire sequence listing.

Example: "<110> APPLICANT: Novartis AG." should be "<110> Novartis AG.".

This type of errors are seen globally throughout the sequences in teh sequence listing. Please make all necessary changes.

<210> SEQ ID NO 46

<211> LENGTH: 239

<212> TYPE: PRT

<213> ORGANISM: Pan paniscus

<400> SEQUENCE: 46

Gly Lys Val Thr Glu Glu Val Val Ala Asn Met Pro Glu Gly Leu Thr
1 5 10 15

Pro Asp Leu Val Gln Glu Ala Cys Glu Ser Glu Leu Asn Glu Val Thr
20 25 30

Gly Thr Lys Ile Ala Tyr Glu Thr Lys Met Asp Leu Val Gln Thr Ser
35 40 45

Glu Val Met Gln Glu Ser Leu Tyr Pro Ala Ala Gln Leu Cys Pro Ser
50 55 60

Phe Glu Glu Ser Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val
65 70 75 80

Met Glu Ala Pro Leu Asn Ser Ala Val Pro Ser Ala Gly Ala Ser Ala
85 90 95
Val Gln Pro Ser Ser Ser Pro Leu Glu Ala Ser Ser Val Asn Tyr Glu
100 105 110
Ser Ile Ile His Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala Met
115 120 125
Ser Val Ser Leu Lys Lys Val Ser Gly Ile Lys Glu Glu Ile Lys Glu
130 135 140
Pro Glu Ser Ile Asn Ala Ala Val Gln Glu Thr Glu Ala Pro Tyr Ile
145 150 155 160
Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Ala Glu Pro
165 170 175
Thr Pro Asp Phe Ser Asp Tyr Ser Glu Met Ala Lys Val Glu Gln Pro
180 185 190
Val Pro Asp His Ser Glu Leu Val Glu Asp Ser Ser Pro Asp Ser Glu
195 200 205
Pro Val Asp Leu Phe Ser Asp Asp Ser Ile Pro Asp Val Pro Gln Lys
210 215 220
Gln Asp Glu Ala Val Met Leu Val Lys Glu Asn Leu Pro Glu Thr
225 230 235

Miss-aligned Amino Acid numbering at position 18 onwards, Please correct
the error.

Application No: 10538201 Version No: 2.0

Input Set:**Output Set:**

Started: 2010-06-09 19:47:41.666
Finished: 2010-06-09 19:47:49.232
Elapsed: 0 hr(s) 0 min(s) 7 sec(s) 566 ms
Total Warnings: 15
Total Errors: 13
No. of SeqIDs Defined: 48
Actual SeqID Count: 48

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (28)
W 213	Artificial or Unknown found in <213> in SEQ ID (29)
W 213	Artificial or Unknown found in <213> in SEQ ID (30)
E 201	Mandatory field data missing in <223> in SEQ ID (30)
W 213	Artificial or Unknown found in <213> in SEQ ID (31)
W 213	Artificial or Unknown found in <213> in SEQ ID (32)
W 213	Artificial or Unknown found in <213> in SEQ ID (33)
W 213	Artificial or Unknown found in <213> in SEQ ID (34)
W 213	Artificial or Unknown found in <213> in SEQ ID (35)
W 213	Artificial or Unknown found in <213> in SEQ ID (36)
W 213	Artificial or Unknown found in <213> in SEQ ID (37)
W 213	Artificial or Unknown found in <213> in SEQ ID (38)
W 213	Artificial or Unknown found in <213> in SEQ ID (39)
W 213	Artificial or Unknown found in <213> in SEQ ID (40)
W 213	Artificial or Unknown found in <213> in SEQ ID (41)
W 213	Artificial or Unknown found in <213> in SEQ ID (42)
E 323	Invalid/missing amino acid numbering SEQID (46) POS (18)
E 323	Invalid/missing amino acid numbering SEQID (46) at Protein (20)
E 323	Invalid/missing amino acid numbering SEQID (46) POS (23)
E 323	Invalid/missing amino acid numbering SEQID (46) at Protein (25)

Input Set:

Output Set:

Started: 2010-06-09 19:47:41.666
Finished: 2010-06-09 19:47:49.232
Elapsed: 0 hr(s) 0 min(s) 7 sec(s) 566 ms
Total Warnings: 15
Total Errors: 13
No. of SeqIDs Defined: 48
Actual SeqID Count: 48

Error code	Error Description
E 323	Invalid/missing amino acid numbering SEQID (46) POS (28)
E 323	Invalid/missing amino acid numbering SEQID (46) at Protein (30)
E 323	Invalid/missing amino acid numbering SEQID (46) POS (33)
E 323	Invalid/missing amino acid numbering SEQID (46) at Protein (35)
E 323	Invalid/missing amino acid numbering SEQID (46) POS (38)
E 323	Invalid/missing amino acid numbering SEQID (46) at Protein (40)
E 323	Invalid/missing amino acid numbering SEQID (46) POS (43)
E 323	Invalid/missing amino acid numbering SEQID (46) at Protein (45)

SEQUENCE LISTING

<110> APPLICANT: Novartis AG
<120> TITLE OF INVENTION: Organic Compound
<130> FILE REFERENCE: 4-32761P1/UNZ

<140> CURRENT APPLICATION NUMBER:10538201
<141> CURRENT FILING DATE:2006-03-08
<160> NUMBER OF SEQ ID NOS: 48
<170> SOFTWARE: PatentIn version 3.1

<210> SEQ ID NO 1
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Rattus norvegicus
<220> FEATURE:
<221> NAME/KEY: PEPTIDE
<222> LOCATION: (1)..(18)
<223> OTHER INFORMATION: rat NogoA_623-640

<400> SEQUENCE: 1
Ser Tyr Asp Ser Ile Lys Leu Glu Pro Glu Asn Pro Pro Pro Tyr Glu
1 5 10 15
Glu Ala

<210> SEQ ID NO 2
<211> LENGTH: 221
<212> TYPE: PRT
<213> ORGANISM: Mus musculus
<220> FEATURE:
<221> NAME/KEY: CHAIN
<222> LOCATION: (1)..(221)
<223> OTHER INFORMATION: Variable part of Heavy Chain of 11C7 with leader sequence
<400> SEQUENCE: 2

Met Asp Phe Gly Leu Ile Phe Phe Ile Val Gly Leu Leu Lys Gly Val
1 5 10 15
Gln Cys Glu Val Lys Leu Leu Glu Ser Gly Gly Leu Val Gln Pro
20 25 30
Gly Gly Ser Leu Lys Leu Ser Cys Val Val Ser Gly Phe Asp Phe Arg
35 40 45
Arg Asn Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
50 55 60
Trp Ile Gly Glu Ile Asn Pro Asp Ser Ser Lys Ile Asn Tyr Thr Pro
65 70 75 80
Ser Leu Lys Asp Lys Phe Ile Ile Ser Arg Asp Asn Ala Lys Asn Thr
85 90 95
Leu Tyr Leu Gln Val Ser Thr Val Arg Ser Glu Asp Thr Ala Leu Tyr
100 105 110
Tyr Cys Val Arg Pro Val Trp Met Tyr Ala Met Asp Tyr Trp Gly Gln
115 120 125
Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val
130 135 140
Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr
145 150 155 160
Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr
165 170 175
Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val

180	185	190
Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser		
195	200	205
Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala		
210	215	220

<210> SEQ ID NO 3
<211> LENGTH: 238
<212> TYPE: PRT
<213> ORGANISM: Mus musculus
<220> FEATURE:
<221> NAME/KEY: CHAIN
<222> LOCATION: (1)..(238)
<223> OTHER INFORMATION: Light Chain of 11C7 with leader sequence
<400> SEQUENCE: 3

Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg Glu		
1	5	10
Thr Ser Gly Asp Val Leu Leu Thr Gln Thr Pro Leu Thr Leu Ser Ile		
20	25	30
Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu		
35	40	45
Leu His Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro		
50	55	60
Gly Gln Ser Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser		
65	70	75
Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr		
85	90	95
Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Leu Tyr Tyr Cys		
100	105	110
Trp Gln Gly Thr His Phe Pro Gln Thr Phe Gly Gly Thr Lys Leu		
115	120	125
Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro		
130	135	140
Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu		
145	150	155
Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly		
165	170	175
Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser		
180	185	190
Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp		
195	200	205
Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr		
210	215	220
Ser Thr Ser Pro Ile Val Lys Ser Phe Asn Arg Gly Glu Cys		
225	230	235

<210> SEQ ID NO 4
<211> LENGTH: 3919
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(3579)
<223> OTHER INFORMATION: Human NogoA
<400> SEQUENCE: 4

atg gaa gac ctg gac cag tct cct ctg gtc tcg tcc tcg gac agc cca

Ser Val Ser Pro Lys Ala Glu Ser Ala Val Ile Val Ala Asn Pro Arg			
305	310	315	320
gaa gaa ata atc gtg aaa aat aaa gat gaa gaa gag aag tta gtt agt			1008
Glu Glu Ile Ile Val Lys Asn Lys Asp Glu Glu Glu Lys Leu Val Ser			
325	330	335	
aat aac atc ctt cat aat caa caa gag tta cct aca gct ctt act aaa			1056
Asn Asn Ile Leu His Asn Gln Gln Glu Leu Pro Thr Ala Leu Thr Lys			
340	345	350	
ttg gtt aaa gag gat gaa gtt gtg tct tca gaa aaa gca aaa gac agt			1104
Leu Val Lys Glu Asp Glu Val Val Ser Ser Glu Lys Ala Lys Asp Ser			
355	360	365	
ttt aat gaa aag aga gtt gca gtg gaa gct cct atg agg gag gaa tat			1152
Phe Asn Glu Lys Arg Val Ala Val Glu Ala Pro Met Arg Glu Glu Tyr			
370	375	380	
gca gac ttc aaa cca ttt gag cga gta tgg gaa gtg aaa gat agt aag			1200
Ala Asp Phe Lys Pro Phe Glu Arg Val Trp Glu Val Lys Asp Ser Lys			
385	390	395	400
gaa gat agt gat atg ttg gct gct gga ggt aaa atc gag agc aac ttg			1248
Glu Asp Ser Asp Met Leu Ala Ala Gly Gly Lys Ile Glu Ser Asn Leu			
405	410	415	
gaa agt aaa gtg gat aaa aaa tgt ttt gca gat agc ctt gag caa act			1296
Glu Ser Lys Val Asp Lys Lys Cys Phe Ala Asp Ser Leu Glu Gln Thr			
420	425	430	
aat cac gaa aaa gat agt gag agt agt aat gat gat act tct ttc ccc			1344
Asn His Glu Lys Asp Ser Glu Ser Ser Asn Asp Asp Thr Ser Phe Pro			
435	440	445	
agt acg cca gaa ggt ata aag gat cgt tca gga gca tat atc aca tgt			1392
Ser Thr Pro Glu Gly Ile Lys Asp Arg Ser Gly Ala Tyr Ile Thr Cys			
450	455	460	
gct ccc ttt aac cca gca gca act gag agc att gca aca aac att ttt			1440
Ala Pro Phe Asn Pro Ala Ala Thr Glu Ser Ile Ala Thr Asn Ile Phe			
465	470	475	480
cct ttg tta gga gat cct act tca gaa aat aag acc gat gaa aaa aaa			1488
Pro Leu Leu Gly Asp Pro Thr Ser Glu Asn Lys Thr Asp Glu Lys Lys			
485	490	495	
ata gaa gaa aag aag gcc caa ata gta aca gag aag aat act agc acc			1536
Ile Glu Glu Lys Ala Gln Ile Val Thr Glu Lys Asn Thr Ser Thr			
500	505	510	
aaa aca tca aac cct ttt ctt gta gca gca cag gat tct gag aca gat			1584
Lys Thr Ser Asn Pro Phe Leu Val Ala Ala Gln Asp Ser Glu Thr Asp			
515	520	525	
tat gtc aca aca gat aat tta aca aag gtg act gag gaa gtc gtg gca			1632
Tyr Val Thr Thr Asp Asn Leu Thr Lys Val Thr Glu Glu Val Val Ala			
530	535	540	
aac atg cct gaa ggc ctg act cca gat tta gta cag gaa gca tgt gaa			1680
Asn Met Pro Glu Gly Leu Thr Pro Asp Leu Val Gln Glu Ala Cys Glu			
545	550	555	560
agt gaa ttg aat gaa gtt act ggt aca aag att gct tat gaa aca aaa			1728
Ser Glu Leu Asn Glu Val Thr Gly Thr Lys Ile Ala Tyr Glu Thr Lys			
565	570	575	
atg gac ttg gtt caa aca tca gaa gtt atg caa gag tca ctc tat cct			1776
Met Asp Leu Val Gln Thr Ser Glu Val Met Gln Glu Ser Leu Tyr Pro			
580	585	590	
gca gca cag ctt tgc cca tca ttt gaa gag tca gaa gct act cct tca			1824
Ala Ala Gln Leu Cys Pro Ser Phe Glu Glu Ser Glu Ala Thr Pro Ser			
595	600	605	
cca gtt ttg cct gac att gtt atg gaa gca cca ttg aat tct gca gtt			1872

Pro Val Leu Pro Asp Ile Val Met Glu Ala Pro Leu Asn Ser Ala Val			
610	615	620	
cct agt gct ggt gct tcc gtg ata cag ccc agc tca tca cca tta gaa			1920
Pro Ser Ala Gly Ala Ser Val Ile Gln Pro Ser Ser Ser Pro Leu Glu			
625	630	635	640
gct tct tca gtt aat tat gaa agc ata aaa cat gag cct gaa aac ccc			1968
Ala Ser Ser Val Asn Tyr Glu Ser Ile Lys His Glu Pro Glu Asn Pro			
645	650	655	
cca cca tat gaa gag gcc atg agt gta tca cta aaa aaa gta tca gga			2016
Pro Pro Tyr Glu Glu Ala Met Ser Val Ser Leu Lys Lys Val Ser Gly			
660	665	670	
ata aag gaa gaa att aaa gag cct gaa aat att aat gca gct ctt caa			2064
Ile Lys Glu Glu Ile Lys Glu Pro Glu Asn Ile Asn Ala Ala Leu Gln			
675	680	685	
gaa aca gaa gct cct tat ata tct att gca tgt gat tta att aaa gaa			2112
Glu Thr Glu Ala Pro Tyr Ile Ser Ile Ala Cys Asp Leu Ile Lys Glu			
690	695	700	
aca aag ctt tct gct gaa cca gct ccg gat ttc tct gat tat tca gaa			2160
Thr Lys Leu Ser Ala Glu Pro Ala Pro Asp Phe Ser Asp Tyr Ser Glu			
705	710	715	720
atg gca aaa gtt gaa cag cca gtg cct gat cat tct gag cta gtt gaa			2208
Met Ala Lys Val Glu Gln Pro Val Pro Asp His Ser Glu Leu Val Glu			
725	730	735	
gat tcc tca cct gat tct gaa cca gtt gac tta ttt agt gat gat tca			2256
Asp Ser Ser Pro Asp Ser Glu Pro Val Asp Leu Phe Ser Asp Asp Ser			
740	745	750	
ata cct gac gtt cca caa aaa caa gat gaa act gtg atg ctt gtg aaa			2304
Ile Pro Asp Val Pro Gln Lys Gln Asp Glu Thr Val Met Leu Val Lys			
755	760	765	
gaa agt ctc act gag act tca ttt gag tca atg ata gaa tat gaa aat			2352
Glu Ser Leu Thr Glu Thr Ser Phe Glu Ser Met Ile Glu Tyr Glu Asn			
770	775	780	
aag gaa aaa ctc agt gct ttg cca cct gag gga gga aag cca tat ttg			2400
Lys Glu Lys Leu Ser Ala Leu Pro Pro Glu Gly Gly Lys Pro Tyr Leu			
785	790	795	800
gaa tct ttt aag ctc agt tta gat aac aca aaa gat acc ctg tta cct			2448
Glu Ser Phe Lys Leu Ser Leu Asp Asn Thr Lys Asp Thr Leu Leu Pro			
805	810	815	
gat gaa gtt tca aca ttg agc aaa aag gag aaa att cct ttg cag atg			2496
Asp Glu Val Ser Thr Leu Ser Lys Lys Glu Lys Ile Pro Leu Gln Met			
820	825	830	
gag gag ctc agt act gca gtt tat tca aat gat gac tta ttt att tct			2544
Glu Glu Leu Ser Thr Ala Val Tyr Ser Asn Asp Asp Leu Phe Ile Ser			
835	840	845	
aag gaa gca cag ata aga gaa act gaa acg ttt tca gat tca tct cca			2592
Lys Glu Ala Gln Ile Arg Glu Thr Glu Thr Phe Ser Asp Ser Ser Pro			
850	855	860	
att gaa att ata gat gag ttc cct aca ttg atc agt tct aaa act gat			2640
Ile Glu Ile Ile Asp Glu Phe Pro Thr Leu Ile Ser Ser Lys Thr Asp			
865	870	875	880
tca ttt tct aaa tta gcc agg gaa tat act gac cta gaa gta tcc cac			2688
Ser Phe Ser Lys Leu Ala Arg Glu Tyr Thr Asp Leu Glu Val Ser His			
885	890	895	
aaa agt gaa att gct aat gcc ccg gat gga gct ggg tca ttg cct tgc			2736
Lys Ser Glu Ile Ala Asn Ala Pro Asp Gly Ala Gly Ser Leu Pro Cys			
900	905	910	
aca gaa ttg ccc cat gac ctt tct ttg aag aac ata caa ccc aaa gtt			2784

Thr Glu Leu Pro His Asp Leu Ser Leu Lys Asn Ile Gln Pro Lys Val

915

920

925

gaa gag aaa